

SEQUENCE LISTING

<110> Donoho, Gregory
 Scoville, John
 Turner, C. Alexander Jr.
 Friedrich, Glenn
 Abuin, Alejandro
 Zambrowicz, Brian
 Sands, Arthur T.

<120> Novel Human Proteases and
 Polynucleotides Encoding the Same

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<151> 2000-02-11

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<213> homo sapiens

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Leu	Gln	Pro	Val	Pro	Glu	Arg	Arg	Ile	Pro	Asn	Arg	Tyr	Leu	Gly	Gln	35	40	45	
Pro	Ser	Pro	Phe	Thr	His	Pro	His	Leu	Leu	Arg	Pro	Gly	Glu	Val	Thr	50	55	60	
Pro	Gly	Leu	Ser	Gln	Val	Glu	Tyr	Ala	Leu	Arg	Arg	His	Lys	Leu	Met	65	70	75	80
Ser	Leu	Ile	Gln	Lys	Glu	Ala	Gln	Gly	Gln	Ser	Gly	Thr	Asp	Gln	Thr	85	90	95	
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Tyr	Thr	Phe	His	Gln	Asp	Asn	Asn	Phe	Leu	Tyr	Leu	Cys	Gly	Phe	Gln	115	120	125	
Glu	Pro	Asp	Ser	Ile	Leu	Val	Leu	Gln	Ser	Leu	Pro	Gly	Lys	Gln	Leu	130	135	140	
Pro	Ser	His	Lys	Ala	Ile	Leu	Phe	Val	Pro	Arg	Arg	Asp	Pro	Ser	Arg	145	150	155	160
Glu	Leu	Trp	Asp	Gly	Pro	Arg	Ser	Gly	Thr	Asp	Gly	Ala	Ile	Ala	Leu	165	170	175	
Thr	Gly	Val	Asp	Glu	Ala	Tyr	Thr	Leu	Glu	Glu	Phe	Gln	His	Leu	Leu	180	185	190	
Pro	Lys	Met	Lys	Val	Leu	Leu	Pro	Ala	Leu	Gln	Lys	Glu	Val	Leu	Phe	195	200	205	
Ser	Lys	Asn	Asp	Pro	Cys	Ile	Thr	Ala	Ser	Glu	Ser	Pro	Ala	Glu	Thr	210	215	220	
Asn	Met	Val	Trp	Tyr	Asp	Trp	Met	Arg	Pro	Ser	His	Ala	Gln	Leu	His	225	230	235	240
Ser	Asp	Tyr	Met	Gln	Pro	Leu	Thr	Glu	Ala	Lys	Ala	Lys	Ser	Lys	Asn	245	250	255	
Lys	Val	Arg	Gly	Val	Gln	Gln	Leu	Ile	Gln	Arg	Leu	Arg	Leu	Ile	Lys	260	265	270	
Ser	Pro	Ala	Glu	Ile	Glu	Arg	Met	Gln	Ile	Ala	Gly	Lys	Leu	Thr	Ser	275	280	285	
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 35 40 45
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 Pro Gly Leu Ser Gln Val Glu Tyr Ala Leu Arg Arg His Lys Leu Met
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 Val Val Val Leu Ser Asn Pro Thr Tyr Met Ser Asn Asp Ile Pro
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 Tyr Thr Phe His Gln Asp Asn Asn Phe Leu Tyr Leu Cys Gly Phe Gln
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 Glu Pro Asp Ser Ile Leu Val Leu Gln Ser Leu Pro Gly Lys Gln Leu
 130 135 140
 Pro Ser His Lys Ala Ile Leu Phe Val Pro Arg Arg Asp Pro Ser Arg
 145 150 155 160
 Glu Leu Trp Asp Gly Pro Arg Ser Gly Thr Asp Gly Ala Ile Ala Leu
 165 170 175
 Thr Gly Val Asp Glu Ala Tyr Thr Leu Glu Glu Phe Gln His Leu Leu
 180 185 190
 Pro Lys Met Lys Ala Glu Thr Asn Met Val Trp Tyr Asp Trp Met Arg
 195 200 205
 Pro Ser His Ala Gln Leu His Ser Asp Tyr Met Gln Pro Leu Thr Glu
 210 215 220
 Ala Lys Ala Lys Ser Lys Asn Lys Val Arg Gly Val Gln Gln Leu Ile
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 35 40 45
 Gln Glu Pro Asp Ser Ile Leu Val Leu Gln Ser Leu Pro Gly Lys Gln
 50 55 60
 Leu Pro Ser His Lys Ala Ile Leu Phe Val Pro Arg Arg Asp Pro Ser
 65 70 75 80
 Arg Glu Leu Trp Asp Gly Pro Arg Ser Gly Thr Asp Gly Ala Ile Ala
 85 90 95
 Leu Thr Gly Val Asp Glu Ala Tyr Thr Leu Glu Glu Phe Gln His Leu
 100 105 110
 Leu Pro Lys Met Lys Val Leu Leu Pro Ala Leu Gln Lys Glu Val Leu
 115 120 125
 Phe Ser Lys Asn Asp Pro Cys Ile Thr Ala Ser Glu Ser Pro Ala Glu
 130 135 140
 Thr Asn Met Val Trp Tyr Asp Trp Met Arg Pro Ser His Ala Gln Leu
 145 150 155 160
 His Ser Asp Tyr Met Gln Pro Leu Thr Glu Ala Lys Ala Lys Ser Lys
 165 170 175
 Asn Lys Val Arg Gly Val Gln Gln Leu Ile Gln Arg Leu Arg Leu Ile
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 35 40 45
 Tyr Ala Leu Arg Arg His Lys Leu Met Ser Leu Ile Gln Lys Glu Ala
 50 55 60
 Gln Gly Gln Ser Gly Thr Asp Gln Thr Val Val Leu Ser Asn Pro
 65 70 75 80
 Thr Tyr Tyr Met Ser Asn Asp Ile Pro Tyr Thr Phe His Gln Asp Asn
 85 90 95
 Asn Phe Leu Tyr Leu Cys Gly Phe Gln Glu Pro Asp Ser Ile Leu Val
 100 105 110
 Leu Gln Ser Leu Pro Gly Lys Gln Leu Pro Ser His Lys Ala Ile Leu
 115 120 125
 Phe Val Pro Arg Arg Asp Pro Ser Arg Glu Leu Trp Asp Gly Pro Arg
 130 135 140
 Ser Gly Thr Asp Gly Ala Ile Ala Leu Thr Gly Val Asp Glu Ala Tyr
 145 150 155 160
 Thr Leu Glu Glu Phe Gln His Leu Leu Pro Lys Met Lys Val Leu Leu
 165 170 175
 Pro Ala Leu Gln Lys Glu Val Leu Phe Ser Lys Asn Asp Pro Cys Ile
 180 185 190
 Thr Ala Ser Glu Ser Pro Ala Glu Thr Asn Met Val Trp Tyr Asp Trp
 195 200 205
 Met Arg Pro Ser His Ala Gln Leu His Ser Asp Tyr Met Gln Pro Leu
 210 215 220
 Thr Glu Ala Lys Ala Lys Ser Lys Asn Lys Val Arg Gly Val Gln Gln

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 Pro Tyr Thr Phe His Gln Asp Asn Asn Phe Leu Tyr Leu Cys Gly Phe
 35 40 45
 Gln Glu Pro Asp Ser Ile Leu Val Leu Gln Ser Leu Pro Gly Lys Gln
 50 55 60
 Leu Pro Ser His Lys Ala Ile Leu Phe Val Pro Arg Arg Asp Pro Ser
 65 70 75 80
 Arg Glu Leu Trp Asp Gly Pro Arg Ser Gly Thr Asp Gly Ala Ile Ala
 85 90 95
 Leu Thr Gly Val Asp Glu Ala Tyr Thr Leu Glu Glu Phe Gln His Leu
 100 105 110
 Leu Pro Lys Met Lys Ala Glu Thr Asn Met Val Trp Tyr Asp Trp Met
 115 120 125
 Arg Pro Ser His Ala Gln Leu His Ser Asp Tyr Met Gln Pro Leu Thr
 130 135 140
 Glu Ala Lys Ala Lys Ser Lys Asn Lys Val Arg Gly Val Gln Gln Leu
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 Ile Gln Arg Leu Arg Leu Ile Lys Ser Pro Ala Glu Ile Glu Arg Met
 165 170 175
 Gln Ile Ala Gly Lys Leu Thr Ser Gln Val
 180 185

<210> 15
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<212> DNA

<213> homo sapiens

<400> 15

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actccaggac tatctcaggt ggaatatgca cttgcgagac acaaactaat gtctctgac      180
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ttaccatcac acaaagccat actttttgtg cctcggcgag atcccagtcg agaactttgg      420
gatggtcgac gatctggcac tgatggagca atagctctaa ctggagtaga cgaagcctat      480
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tatgactgga tgaggccctc acatgcacag cttcactctg actatatgca gcccctgact      600
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<400> 16

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His Leu Leu Arg Pro Gly Glu Val Thr Pro Gly Leu Ser Gln Val Glu
          35           40           45
Tyr Ala Leu Arg Arg His Lys Leu Met Ser Leu Ile Gln Lys Glu Ala
          50           55           60
Gln Gly Gln Ser Gly Thr Asp Gln Thr Val Val Val Leu Ser Asn Pro
65           70           75           80
Thr Tyr Tyr Met Ser Asn Asp Ile Pro Tyr Thr Phe His Gln Asp Asn
          85           90           95
Asn Phe Leu Tyr Leu Cys Gly Phe Gln Glu Pro Asp Ser Ile Leu Val
          -100           -105           110
Leu Gln Ser Leu Pro Gly Lys Gln Leu Pro Ser His Lys Ala Ile Leu
          115           120           125
Phe Val Pro Arg Arg Asp Pro Ser Arg Glu Leu Trp Asp Gly Pro Arg
          130           135           140
Ser Gly Thr Asp Gly Ala Ile Ala Leu Thr Gly Val Asp Glu Ala Tyr
145           150           155           160
Thr Leu Glu Glu Phe Gln His Leu Leu Pro Lys Met Lys Ala Glu Thr
          165           170           175
Asn Met Val Trp Tyr Asp Trp Met Arg Pro Ser His Ala Gln Leu His
          180           185           190
Ser Asp Tyr Met Gln Pro Leu Thr Glu Ala Lys Ala Lys Ser Lys Asn
          195           200           205
Lys Val Arg Gly Val Gln Gln Leu Ile Gln Arg Leu Arg Leu Ile Lys
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Gln Val
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 <213> homo sapiens

<400> 17

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aatttcctgt	acctatgtgg	attccaagag	cctgatagca	ttcttgtcct	tcagagcctc	180
cctggcaaac	aattaccatc	acacaaagcc	atactttttg	tgcctcggcg	agatcccagt	240
cgagaacttt	gggatgggcc	gcgatctggc	actgatggag	caatagctct	aactggagta	300
gacgaagcct	atacgctaga	agaatttcaa	catcttctac	caaaaatgaa	agtgtctctg	360
ccagctcttc	aaaaggaggt	actgttctcc	aagaacgac	catgcatcac	agcatcagaa	420
tcacctgctg	agacgaacat	ggtttggtat	gactggatga	ggccctcaca	tgcacagctt	480
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gcccctgtgg	aagaagcctt	tctttatgct	aagtttgaat	ttgaatgccg	ggctcgtggc	720
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gcacctcagg	cagaactcta	tgaagccgtt	ctagagatcc	aaagagattg	tttggccctc	960
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cgaaaatact	gtcctcatca	tgttggccac	tacctcggga	tggatgtcca	tgacactcca	1140
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tatattccag	aggatgacaa	agatgcccc	gagaagtttc	ggggtcttgg	tgtacgaatt	1260
gaggatgatg	tagtgggtgac	tcaggactca	cctctcatcc	tttctgcaga	ctgtcccaaa	1320
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<210> 18
 <211> 453
 <212> PRT
 <213> homo sapiens

<400> 18

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			20					25					30		
Pro	Tyr	Thr	Phe	His	Gln	Asp	Asn	Asn	Phe	Leu	Tyr	Leu	Cys	Gly	Phe
		35				40					45				
Gln	Glu	Pro	Asp	Ser	Ile	Leu	Val	Leu	Gln	Ser	Leu	Pro	Gly	Lys	Gln
	50					55				60					
Leu	Pro	Ser	His	Lys	Ala	Ile	Leu	Phe	Val	Pro	Arg	Arg	Asp	Pro	Ser
65				70					75				80		
Arg	Glu	Leu	Trp	Asp	Gly	Pro	Arg	Ser	Gly	Thr	Asp	Gly	Ala	Ile	Ala
			85					90					95		
Leu	Thr	Gly	Val	Asp	Glu	Ala	Tyr	Thr	Leu	Glu	Glu	Phe	Gln	His	Leu
		100					105						110		
Leu	Pro	Lys	Met	Lys	Val	Leu	Leu	Pro	Ala	Leu	Gln	Lys	Glu	Val	Leu
	115					120					125				
Phe	Ser	Lys	Asn	Asp	Pro	Cys	Ile	Thr	Ala	Ser	Glu	Ser	Pro	Ala	Glu
	130					135				140					
Thr	Asn	Met	Val	Trp	Tyr	Asp	Trp	Met	Arg	Pro	Ser	His	Ala	Gln	Leu
145					150				155					160	

His Ser Asp Tyr Met Gln Pro Leu Thr Glu Ala Lys Ala Lys Ser Lys
 165 170 175
 Asn Lys Val Arg Gly Val Gln Gln Leu Ile Gln Arg Leu Arg Leu Ile
 180 185 190
 Lys Ser Pro Ala Glu Ile Glu Arg Met Gln Ile Ala Gly Lys Leu Thr
 195 200 205
 Ser Gln Ala Phe Ile Glu Thr Met Phe Thr Ser Lys Ala Pro Val Glu
 210 215 220
 Glu Ala Phe Leu Tyr Ala Lys Phe Glu Phe Glu Cys Arg Ala Arg Gly
 225 230 235 240
 Ala Asp Ile Leu Ala Tyr Pro Pro Val Val Ala Gly Gly Asn Arg Ser
 245 250 255
 Asn Thr Leu His Tyr Val Lys Asn Asn Gln Leu Ile Lys Asp Gly Glu
 260 265 270
 Met Val Leu Leu Asp Gly Gly Cys Glu Ser Ser Cys Tyr Val Ser Asp
 275 280 285
 Ile Thr Arg Thr Trp Pro Val Asn Gly Arg Phe Thr Ala Pro Gln Ala
 290 295 300
 Glu Leu Tyr Glu Ala Val Leu Glu Ile Gln Arg Asp Cys Leu Ala Leu
 305 310 315 320
 Cys Phe Pro Gly Thr Ser Leu Glu Asn Ile Tyr Ser Met Met Leu Thr
 325 330 335
 Leu Ile Gly Gln Lys Leu Lys Asp Leu Gly Ile Met Lys Asn Ile Lys
 340 345 350
 Glu Asn Asn Ala Phe Lys Ala Ala Arg Lys Tyr Cys Pro His His Val
 355 360 365
 Gly His Tyr Leu Gly Met Asp Val His Asp Thr Pro Asp Met Pro Arg
 370 375 380
 Ser Leu Pro Leu Gln Pro Gly Met Val Ile Thr Ile Glu Pro Gly Ile
 385 390 395 400
 Tyr Ile Pro Glu Asp Asp Lys Asp Ala Pro Glu Lys Phe Arg Gly Leu
 405 410 415
 Gly Val Arg Ile Glu Asp Asp Val Val Val Thr Gln Asp Ser Pro Leu
 420 425 430
 Ile Leu Ser Ala Asp Cys Pro Lys Glu Met Asn Asp Ile Glu Gln Ile
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 Cys Ser Gln Ala Ser
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<210> 19
 <211> 1599
 <212> DNA
 <213> homo sapiens

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 attccaaacc gatacttagg ccagcccagc cccctttacac acccacacct cctcagacca 180
 ggggaggtta ctccaggact atctcaggtg gaatatgcac ttgcgagaca caaactaatg 240
 tctctgatcc agaagggaagc tcaagggcag agtgggacag accagacagt ggttgtgctc 300
 tccaacccta catactacat gagcaacgat attccctata ctttcacca agacaacaat 360
 ttctgtacc tatgtggatt ccaagagcct gatagcattc ttgtccttca gaggctccct 420
 ggcaacaat taccatcaca caaagccata ctttttgtgc ctgcgcgaga tcccagtcga 480
 gaactttggg atgggtccgcg atctggcact gatggagcaa tagctctaac tggagtagac 540
 gaagcctata cgctagaaga atttcaacat cttctaccaa aaatgaaagt gctcttgcca 600
 gctcttcaaa aggaggtact gttctccaag aacgatccat gcacacagc atcagaatca 660

cctgctgaga	cgaacatggt	ttggtatgac	tggatgaggc	cctcacatgc	acagcttcac	720
tctgactata	tgagccct	gactgaggcc	aaagccaaga	gcaagaacaa	ggttcggggt	780
gttcagcagc	tgatacagcg	cctccggctg	atcaagtctc	ctgcagaaat	tgaacgaatg	840
cagattgctg	ggaagctgac	atcacaggct	ttcatagaaa	ccatgttcac	cagtaaagcc	900
cctgtggaag	aagcctttct	ttatgctaag	tttgaatttg	aatgccgggc	tcgtggcgca	960
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gtgaaaaata	atcaactcat	caaggatggg	gaaatggtgc	ttctggatgg	aggttgtgag	1080
tcttcctgct	atgtgagtga	catcacacgt	acgtggccag	tcaatggcag	gttcaccgca	1140
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ttccctggga	caagcttggg	gaacatctac	agcatgatgc	tgaccctgat	aggacagaag	1260
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aaatactgtc	ctcatcatgt	tggccactac	ctcgggatgg	atgtccatga	cactccagac	1380
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attccagagg	atgacaaaga	tgccccagag	aagtttcggg	gtcttggtgt	acgaattgag	1500
gatgatgtag	tggtgactca	ggactcacct	ctcatccttt	ctgcagactg	tcccaaagag	1560
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<210> 20

<211> 532

<212> PRT

<213> homo sapiens

<400> 20

Met	Pro	Trp	Leu	Leu	Ser	Ala	Pro	Lys	Leu	Val	Pro	Ala	Val	Ala	Asn
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Val	Arg	Gly	Leu	Ser	Gly	Cys	Met	Leu	Cys	Ser	Gln	Arg	Arg	Tyr	Ser
			20					25					30		
Leu	Gln	Pro	Val	Pro	Glu	Arg	Arg	Ile	Pro	Asn	Arg	Tyr	Leu	Gly	Gln
			35				40					45			
Pro	Ser	Pro	Phe	Thr	His	Pro	His	Leu	Leu	Arg	Pro	Gly	Glu	Val	Thr
	50					55				60					
Pro	Gly	Leu	Ser	Gln	Val	Glu	Tyr	Ala	Leu	Arg	His	Lys	Leu	Met	
65					70					75				80	
Ser	Leu	Ile	Gln	Lys	Glu	Ala	Gln	Gly	Gln	Ser	Gly	Thr	Asp	Gln	Thr
			85					90					95		
Val	Val	Val	Leu	Ser	Asn	Pro	Thr	Tyr	Tyr	Met	Ser	Asn	Asp	Ile	Pro
			100					105					110		
Tyr	Thr	Phe	His	Gln	Asp	Asn	Asn	Phe	Leu	Tyr	Leu	Cys	Gly	Phe	Gln
			115				120					125			
Glu	Pro	Asp	Ser	Ile	Leu	Val	Leu	Gln	Ser	Leu	Pro	Gly	Lys	Gln	Leu
			130				135					140			
Pro	Ser	His	Lys	Ala	Ile	Leu	Phe	Val	Pro	Arg	Arg	Asp	Pro	Ser	Arg
145					150					155				160	
Glu	Leu	Trp	Asp	Gly	Pro	Arg	Ser	Gly	Thr	Asp	Gly	Ala	Ile	Ala	Leu
			165					170					175		
Thr	Gly	Val	Asp	Glu	Ala	Tyr	Thr	Leu	Glu	Glu	Phe	Gln	His	Leu	Leu
			180					185				190			
Pro	Lys	Met	Lys	Val	Leu	Leu	Pro	Ala	Leu	Gln	Lys	Glu	Val	Leu	Phe
			195				200					205			
Ser	Lys	Asn	Asp	Pro	Cys	Ile	Thr	Ala	Ser	Glu	Ser	Pro	Ala	Glu	Thr
			210			215				220					
Asn	Met	Val	Trp	Tyr	Asp	Trp	Met	Arg	Pro	Ser	His	Ala	Gln	Leu	His
225					230					235				240	
Ser	Asp	Tyr	Met	Gln	Pro	Leu	Thr	Glu	Ala	Lys	Ala	Lys	Ser	Lys	Asn
			245					250				255			
Lys	Val	Arg	Gly	Val	Gln	Gln	Leu	Ile	Gln	Arg	Leu	Arg	Leu	Ile	Lys

260	265	270
Ser Pro Ala Glu Ile Glu Arg Met Gln Ile Ala Gly Lys Leu Thr Ser		
275	280	285
Gln Ala Phe Ile Glu Thr Met Phe Thr Ser Lys Ala Pro Val Glu Glu		
290	295	300
Ala Phe Leu Tyr Ala Lys Phe Glu Phe Glu Cys Arg Ala Arg Gly Ala		
305	310	315
Asp Ile Leu Ala Tyr Pro Pro Val Val Ala Gly Gly Asn Arg Ser Asn		
325	330	335
Thr Leu His Tyr Val Lys Asn Asn Gln Leu Ile Lys Asp Gly Glu Met		
340	345	350
Val Leu Leu Asp Gly Gly Cys Glu Ser Ser Cys Tyr Val Ser Asp Ile		
355	360	365
Thr Arg Thr Trp Pro Val Asn Gly Arg Phe Thr Ala Pro Gln Ala Glu		
370	375	380
Leu Tyr Glu Ala Val Leu Glu Ile Gln Arg Asp Cys Leu Ala Leu Cys		
385	390	400
Phe Pro Gly Thr Ser Leu Glu Asn Ile Tyr Ser Met Met Leu Thr Leu		
405	410	415
Ile Gly Gln Lys Leu Lys Asp Leu Gly Ile Met Lys Asn Ile Lys Glu		
420	425	430
Asn Asn Ala Phe Lys Ala Ala Arg Lys Tyr Cys Pro His His Val Gly		
435	440	445
His Tyr Leu Gly Met Asp Val His Asp Thr Pro Asp Met Pro Arg Ser		
450	455	460
Leu Pro Leu Gln Pro Gly Met Val Ile Thr Ile Glu Pro Gly Ile Tyr		
465	470	475
Ile Pro Glu Asp Asp Lys Asp Ala Pro Glu Lys Phe Arg Gly Leu Gly		
485	490	495
Val Arg Ile Glu Asp Asp Val Val Val Thr Gln Asp Ser Pro Leu Ile		
500	505	510
Leu Ser Ala Asp Cys Pro Lys Glu Met Asn Asp Ile Glu Gln Ile Cys		
515	520	525
Ser Gln Ala Ser		
530		

<210> 21
 <211> 1287
 <212> DNA
 <213> homo sapiens

<400> 21

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aatttcctgt acctatgtgg attccaagag cctgatagca ttcttgtcct tcagagcctc	180
cctggcaaac aattaccatc acacaaagcc atactttttg tgcctcggcg agatcccagt	240
cgagaacttt gggatggtcc gcgatctggc actgatggag caatagctct aactggagta	300
gacgaagcct atacgctaga agaatttcaa catcttctac caaaaatgaa agctgagacg	360
aacatggttt ggtatgactg gatgaggccc tcacatgcac agcttcactc tgactatatg	420
cagcccctga ctgaggccaa agccaagagc aagaacaagg ttcgggggtg tccagcagctg	480
atacagcgcc tccggctgat caagtctcct gcagaaattg aacgaatgca gattgctggg	540
aagctgacat cacaggcttt catagaaacc atgttcacca gtaaagcccc tgtggaagaa	600
gcctttcttt atgctaagtt tgaatttgaa tgccgggctc gtggcgagaa cattttagcc	660
tatccacctg tggatggctg tggtaatcgg tcaaacactt tgcactatgt gaaaaataat	720
caactcatca aggatgggga aatggtgctt ctggatggag gttgtgagtc ttctgtctat	780
gtgagtgcac tcacacgtac gtggccagtc aatggcaggt tcaccgcacc tcaggcagaa	840

ctctatgaag ccgttctaga gatccaaaga gattgtttgg ccctctgctt ccctgggaca 900
agcttggaga acatctacag catgatgctg accctgatag gacagaagct taaagacttg 960
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gaacagatat gcagccaggc ttcttga 1287

<210> 22

<211> 428

<212> PRT

<213> homo sapiens

<400> 22

Met	Ser	Leu	Ile	Gln	Lys	Glu	Ala	Gln	Gly	Gln	Ser	Gly	Thr	Asp	Gln	
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Thr	Val	Val	Val	Leu	Ser	Asn	Pro	Thr	Tyr	Tyr	Met	Ser	Asn	Asp	Ile	
				20				25					30			
Pro	Tyr	Thr	Phe	His	Gln	Asp	Asn	Asn	Phe	Leu	Tyr	Leu	Cys	Gly	Phe	
				35			40					45				
Gln	Glu	Pro	Asp	Ser	Ile	Leu	Val	Leu	Gln	Ser	Leu	Pro	Gly	Lys	Gln	
				50		55					60					
Leu	Pro	Ser	His	Lys	Ala	Ile	Leu	Phe	Val	Pro	Arg	Arg	Asp	Pro	Ser	
65				70						75				80		
Arg	Glu	Leu	Trp	Asp	Gly	Pro	Arg	Ser	Gly	Thr	Asp	Gly	Ala	Ile	Ala	
				85					90					95		
Leu	Thr	Gly	Val	Asp	Glu	Ala	Tyr	Thr	Leu	Glu	Glu	Phe	Gln	His	Leu	
				100				105					110			
Leu	Pro	Lys	Met	Lys	Ala	Glu	Thr	Asn	Met	Val	Trp	Tyr	Asp	Trp	Met	
				115			120					125				
Arg	Pro	Ser	His	Ala	Gln	Leu	His	Ser	Asp	Tyr	Met	Gln	Pro	Leu	Thr	
				130		135					140					
Glu	Ala	Lys	Ala	Lys	Ser	Lys	Asn	Lys	Val	Arg	Gly	Val	Gln	Gln	Leu	
145				150						155					160	
Ile	Gln	Arg	Leu	Arg	Leu	Ile	Lys	Ser	Pro	Ala	Glu	Ile	Glu	Arg	Met	
				165					170					175		
Gln	Ile	Ala	Gly	Lys	Leu	Thr	Ser	Gln	Ala	Phe	Ile	Glu	Thr	Met	Phe	
				180				185					190			
Thr	Ser	Lys	Ala	Pro	Val	Glu	Glu	Ala	Phe	Leu	Tyr	Ala	Lys	Phe	Glu	
				195			200					205				
Phe	Glu	Cys	Arg	Ala	Arg	Gly	Ala	Asp	Ile	Leu	Ala	Tyr	Pro	Pro	Val	
				210		215					220					
Val	Ala	Gly	Gly	Asn	Arg	Ser	Asn	Thr	Leu	His	Tyr	Val	Lys	Asn	Asn	
225				230						235				240		
Gln	Leu	Ile	Lys	Asp	Gly	Glu	Met	Val	Leu	Leu	Asp	Gly	Gly	Cys	Glu	
				245					250					255		
Ser	Ser	Cys	Tyr	Val	Ser	Asp	Ile	Thr	Arg	Thr	Trp	Pro	Val	Asn	Gly	
				260				265					270			
Arg	Phe	Thr	Ala	Pro	Gln	Ala	Glu	Leu	Tyr	Glu	Ala	Val	Leu	Glu	Ile	
				275			280					285				
Gln	Arg	Asp	Cys	Leu	Ala	Leu	Cys	Phe	Pro	Gly	Thr	Ser	Leu	Glu	Asn	
				290		295					300					
Ile	Tyr	Ser	Met	Met	Leu	Thr	Leu	Ile	Gly	Gln	Lys	Leu	Lys	Asp	Leu	
305				310						315				320		
Gly	Ile	Met	Lys	Asn	Ile	Lys	Glu	Asn	Asn	Ala	Phe	Lys	Ala	Ala	Arg	

325 330 335
 Lys Tyr Cys Pro His His Val Gly His Tyr Leu Gly Met Asp Val His
 340 345 350
 Asp Thr Pro Asp Met Pro Arg Ser Leu Pro Leu Gln Pro Gly Met Val
 355 360 365
 Ile Thr Ile Glu Pro Gly Ile Tyr Ile Pro Glu Asp Asp Lys Asp Ala
 370 375 380
 Pro Glu Lys Phe Arg Gly Leu Gly Val Arg Ile Glu Asp Asp Val Val
 385 390 395 400
 Val Thr Gln Asp Ser Pro Leu Ile Leu Ser Ala Asp Cys Pro Lys Glu
 405 410 415
 Met Asn Asp Ile Glu Gln Ile Cys Ser Gln Ala Ser
 420 425

<210> 23
 <211> 1530
 <212> DNA
 <213> homo sapiens

<400> 23
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 actccaggac tatctcaggt ggaatatgca cttcgagac acaaactaat gtctctgac 180
 cagaaggaag ctcaaggga gagtgggaca gaccagacag tggttgtgct ctccaaccct 240
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 gatggtccgc gatctggcac tgatggagca atagctctaa ctggagtaga cgaagcctat 480
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 attgaacaga tatgcagcca ggcttcttga 1530

<210> 24
 <211> 509
 <212> PRT
 <213> homo sapiens

<400> 24
 Met Leu Cys Ser Gln Arg Arg Tyr Ser Leu Gln Pro Val Pro Glu Arg
 1 5 10 15
 Arg Ile Pro Asn Arg Tyr Leu Gly Gln Pro Ser Pro Phe Thr His Pro

			20					25					30			
His	Leu	Leu	Arg	Pro	Gly	Glu	Val	Thr	Pro	Gly	Leu	Ser	Gln	Val	Glu	
		35					40					45				
Tyr	Ala	Leu	Arg	Arg	His	Lys	Leu	Met	Ser	Leu	Ile	Gln	Lys	Glu	Ala	
	50					55					60					
Gln	Gly	Gln	Ser	Gly	Thr	Asp	Gln	Thr	Val	Val	Val	Leu	Ser	Asn	Pro	
65					70					75					80	
Thr	Tyr	Tyr	Met	Ser	Asn	Asp	Ile	Pro	Tyr	Thr	Phe	His	Gln	Asp	Asn	
				85				90						95		
Asn	Phe	Leu	Tyr	Leu	Cys	Gly	Phe	Gln	Glu	Pro	Asp	Ser	Ile	Leu	Val	
		100						105					110			
Leu	Gln	Ser	Leu	Pro	Gly	Lys	Gln	Leu	Pro	Ser	His	Lys	Ala	Ile	Leu	
		115					120					125				
Phe	Val	Pro	Arg	Arg	Asp	Pro	Ser	Arg	Glu	Leu	Trp	Asp	Gly	Pro	Arg	
	130	-				135					140					
Ser	Gly	Thr	Asp	Gly	Ala	Ile	Ala	Leu	Thr	Gly	Val	Asp	Glu	Ala	Tyr	
145					150					155					160	
Thr	Leu	Glu	Glu	Phe	Gln	His	Leu	Leu	Pro	Lys	Met	Lys	Val	Leu	Leu	
				165					170					175		
Pro	Ala	Leu	Gln	Lys	Glu	Val	Leu	Phe	Ser	Lys	Asn	Asp	Pro	Cys	Ile	
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Gln Gly Gln Ser Gly Thr Asp Gln Thr Val Val Leu Ser Asn Pro
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Thr Tyr Tyr Met Ser Asn Asp Ile Pro Tyr Thr Phe His Gln Asp Asn
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